

SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: Fred Hutchinson Cancer Research Center, Inc.  
 (B) STREET: 1100 Fairview Avenue North, Mailstop c2M-027  
 (C) CITY: Seattle  
 (D) STATE: Washington  
 (E) COUNTRY: USA  
 (F) POSTAL CODE (ZIP): 98109

(A) NAME: Thomas Spies  
 (B) STREET: 2429 E. Aloha  
 (C) CITY: Seattle  
 (D) STATE: Washington  
 (E) COUNTRY: USA  
 (F) POSTAL CODE (ZIP): 98112

(A) NAME: Veronika Spies  
 (B) STREET: 2429 E. Aloha  
 (C) CITY: Seattle  
 (D) STATE: Washington  
 (E) COUNTRY: USA  
 (F) POSTAL CODE (ZIP): 98112

(ii) TITLE OF INVENTION: CELL STRESS REGULATED HUMAN MHC CLASS I GENE

(iii) NUMBER OF SEQUENCES: 16

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/029,044  
 (B) FILING DATE: 29-OCT-1996

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11722 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CACTGCTTGA GCCGCTGAGA GGGTGGCGAC GTCGGGGCCA TGGGGCTGGG CCCGGTCTTC	60
CTGCTTCTGG CTGGCATCTT CCCTTTTGCA CCTCCGGGAG CTGCTGCTGG TGAGTGGCGT	120
TCCTGGCGGT CCTCGGCGGA GCGGGAGCAG TGGGACGTTT CCGGGGGTCG GGTGGGTAGC	180
GGCGAGCGCT GTGCGGTCAG GCGGGGGCTC CTGTGCCCTG TCGGTGGCGC AGGGAGCTGG	240

ACGGGGCCCG	TTACCGCCAC	ACTTCAGCCC	TGCTTCCCCG	TCACTTTTC	GTCTCTCTCG	300
GGATCGCGCA	TCACCTGCAC	TTTCTGGTCT	CCTCCTGCTC	TTTCTCTCCT	CGCGTCTCCT	360
CCGCTTCTCT	TCACTTTTCG	GACAAACCAG	TCCTTCTGAG	GCCCATGGGT	TCCCGGGCTG	420
CCTCCGGGGC	TGCTCCTGTG	AATGGCATT	GAGTGCCCTT	CCAGCGCGGC	CACTGAAGCA	480
GCCACAACCC	CCGGTGCTCG	GGGCGGCTCT	CAGGTCCCTG	AAGTCCTGTC	CTCTCCCGGA	540
GCCGACGTGT	TCTCAGCTCC	TGGGCCGAG	CTCCTGGAGT	AGGGGCCCTC	CTTCTCGGG	600
ACCCGGAGCT	GGTGCTTCCT	GCTGCTGTGG	GGACTGTGGG	GGGTCCTGAC	TCTCAAGCTG	660
AGGGGTGGA	GTCTGCAGGC	TCCGGGCAGA	GGATTCTTCC	TGCGACTTCT	CTCATCCCCA	720
GCTCATTCTC	CCCTCGCCTC	TGGCTCCGAG	GGTCTCTTCC	TCTCTCTCAT	CCCACCCCTA	780
CTAATGACCA	GTGATCTAAG	GACACCAGAT	TCCCTCTCAC	CTCCTCCCTG	CCCATCTCAG	840
GGCCCGCTGA	GTCTTTTTCG	CCTCCAGCT	CCCTGCTACC	CCTTCCTGTG	TGCTGTTCTC	900
TGATCCATTT	CTAGGGTGTC	CTCTGCCCTC	ATCCCCTGTC	CCCGCCACCG	AAGTCCCTCC	960
TGCACCCCTT	ATGGGCCTTT	CCTACAAGCA	GCCTTCACCC	AGTGCTGCCC	CTATGCCTCC	1020
CCGTTCCCAA	ATGTCCCTGA	CTCTAACTTT	CTGGTGCTGC	CTTTTATCCG	GGGGGGTCTT	1080
CCCTCCATCC	CACTCCCTC	CAGACCCCA	AGGGGAACCC	TGATGCTAAT	GGCAGTTGGG	1140
CCTTAGGCAG	GGCGCAGGGC	AGCGCAGATG	CCCCCTCCCC	TCCAGTGACG	ATGCCTGTTC	1200
TGGACCCTGC	CTCATTGTGG	CCCCTTCCCC	ACTCCTTCAT	CCTCAGCCTC	ACCCTCTTGA	1260
GGACCCACCC	CTCCAGCCCA	CAGGTGCTGG	ACCATCCCTC	CCTGGTCCCT	CCGCCCCCTC	1320
CCACCTTGGG	ACCTTGTGCT	GCTCCTATCT	CTTGCCGAGC	TGCCTTGGGC	CCTCAGCAGG	1380
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TCCCACAGTC	ACTCCTGCCC	CATGCTCATG	CCGCCCTCCA	GTTCTTGCTC	TGCCCATCTC	1560
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CTTCCTCAGG	CTGAGAATCT	CCCCCTCTAC	CTTGGTTTTC	TCTCTCTGGC	CAGCACCCCC	1800
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TATATTTATG	GGGTACATGG	GATATTTTGA	CACAGGCCTA	CAATATGTAA	TAATCACATC	1920
AGGGTAAATG	GGTTATATCA	CAACAAGCAT	TTATCCTTTC	TTGTGCTAC	AAACAATCCC	1980

ATTATGCTCT	TTCAGTTATT	TTTAAATGTA	CAATAAATTA	TTGTTGACTG	TACTCACCCCT	2040
GCTGTGCTAT	CTACTAGATC	TTATTCAATC	TAATTATATT	TTTGTACCCA	TTATTAAACCA	2100
TCCCTGCTCC	CCCACTCCCC	ACTACCCTTC	TCAGCCTCTG	GTAATCATCA	TTCTATTGTC	2160
TCTCCCCATG	AGGTCCATTG	TTTTAAATTT	TGGCTGCCAC	AAATAAGTGA	GAACATGCAA	2220
AGTTTGTCTG	TCTGGGCCTG	GGGCTTATTT	CAC TTCACAG	GATGACCTCC	AGTTCTTTGC	2280
AAATGACACG	ATGGCTGAAT	AGTTCTCCAC	ATACACATGT	ACACCACATT	TTCTTTATCC	2340
ATGCGTCTGT	TGATGGACAC	TTAGATTGCT	TGCAGATCTT	GGCTACTTTG	AATAGTGCTG	2400
CAATAAACAT	GGAAAAGTAG	ATAGCTCTTT	AATATACCGA	TTTCCTTTCT	TTGGAGTATA	2460
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GAACCTCCAC	ATTGTTTCCC	ATAGTG GTTG	TACTAGTTTA	CGTTCACCAC	AACAGTGTAC	2580
ATCCTCACCA	GCATTCCTTA	TTTCTACATC	CTCGCCAGCA	TTCTTTATTG	CCTGTCTTCT	2640
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ATCTGTTGAC	GAATGATGTT	GAGCACCTTT	TCATATACCT	GTTTGCCATT	TATATGTCTT	2760
CTTTTGAGAA	ATGACTATTC	AGATCTTTTC	TCATTTTTAA	ATTGGATTAT	TATATTTTTT	2820
TTCTTATAGT	TGTTGAGCT	CCTTATATGT	TTCAGTTACT	GATCCTTTGT	CAGATGAATA	2880
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GCTGTGCAGA	AGCCTTTTTA	CTTGATATGA	TCCCATTTAT	GCAATTTTAC	TTTGGTTACC	3000
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CCAATGTTTT	CTTG TATAGT	TTCATAGTTT	GAGGTCATAG	ATTTACATCT	TTAATCCACT	3120
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TATCTAGTTT	CCCCAGCACC	ATTTTTGAAG	AGACTCTCCT	TTGCCAATGT	GTGTTCTTGG	3240
TACCTTTGTT	GGAAATGAGT	TTACTGTAGA	TGTATGGAAT	TGTTTCTGGG	TTCTCTATTC	3300
TGTTTCATTG	GTCTGTGTGT	CTGTTTTTAT	GCCAGTATCA	TGCTGTTTTG	GTTACTGTAG	3360
CTCTGTAGTA	TAATTTGAAG	TCAGATAATG	TGATTCCTCT	AGTTTTGTTC	ATTTTGCTCA	3420
GGATAGCTTT	ATCTATTCTG	GTTTTTTTGT	GGTTCCATAT	GCATTTTAGG	ATTATTTTTA	3480
TTATTTCTGT	GAAGAATGTC	ATTAGTGTTT	TGATAGGGAT	TGCATTGAAT	CTGTAGATTA	3540
CTTTGGG TAG	TATGGATATT	TCAACAAAAC	TGATTCTTCC	AATCCATGAA	CGTGGACTAT	3600
CTTTTCATT	TTTTGTGTCC	TTCAATTTTT	TGCATCAGTG	TTTTTTGTTT	TTGGTTTTTG	3660
AGATGGAGTT	TCACTCTTGT	TGCCCAGGCT	AGAATGCAAG	GGTGTGATCT	TGGCTCACCG	3720

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

CCAAGTTGTA GTATGGGTCA GAATTTTCATT CCTTTTAAGG ATGGATAATA CTCATTATAT	5520
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TTTGCCAACC TTGCTCTGTG TGTGTGTGTA TGTGTGTGTG TAGGTGTGTG ATAACAGCCA	5760
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GCATAGATGT TTTGAATTTT CATCAGTCTA CTTTGTCACT TCTTTCTATT CTATCTGTGC	6060
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CTGCCCCCAG AACTATTTGC TGAAAAGATC AACTGACTCT TTGTCACCTG CTCACCCCAG	6300
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CCTATGCACC ACAGCCACAC TGGACATGGG TCCCTCTGAG CCTGAGTCCC TTCCCATTC	6600
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GGGGTCAGTG	GAAGTCAGCA	GGGAGGTGAG	CCGGCACTCA	GCCCCACACAG	GGAGGCATGG	7380
GGGAGGGCCA	GGGAGGCGTA	CCCCCTGGGC	TGAGTTCCTC	ACTTGGGTGG	AAAGGTGATG	7440
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TAGGGTCTGT	GAGATCCATG	AAGACAACAG	CACCAGGAGC	TCCCAGCATT	TCTACTACGA	7560
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TGAGGACAGA	CTTGCAGGTC	AGGGGTCCCG	GAGGGCTTCA	GCCAGAGTGA	GAACAGTGAA	8280
GAGAAACAGC	CCTGTTCTCT	TCCCCCTCCT	AGAGGGGAGC	AGGGCTTCAC	TGGCTCTGCC	8340
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ATCACCGTGA	CATGCAGGGC	TTCCAGCTTC	TATCCCCGGA	ATATCACACT	GACCTGGCGT	8460
CAGGATGGGG	TATCTTTGAG	CCACGACACC	CAGCAGTGGG	GGGATGTCCT	GCCTGATGGG	8520
AATGGAACCT	ACCAGACCTG	GGTGGCCACC	AGGATTTGCC	AAGGAGAGGA	GCAGAGGTTC	8580
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GGTGGGGTGA	GCTGGGAATC	ACGTGCTGAA	TGCTGAGGGC	CTGGATGATC	ACGGCCTCAG	9240
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ACCATTGAG	GCCCTACTCT	TTCCAGGTTT	CCACGGCCTG	GCCTCCCTGA	GTTTCTTGCA	9600
GATGACATGG	ATGAGTAGAT	AAGCAGATGT	CCCTGGGCCA	TTTGAGGAGT	GGGGCCCAGC	9660
CCCTCATCAG	GGCAGCTGTG	GTCCCTGTTT	TCATCTACC	TCCGAGTGTT	TTCTTCTCCA	9720
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AAAAGAGACA	GCAGGAAGTT	TTGTGTTTCT	GCAAAGACAG	AAGCAGTTCA	GGCGACAGTA	9960
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GCCCTGCAGC	AAGAGGGCCC	TGTCCAGGAG	GCACCCACAA	CAGAGGCAGT	GCAGGTCTGT	10140
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GTGGGCAGGA	ATGGTTTCCT	CATAGGTCAC	TGGAGTTTTG	GCCAGGAAAA	GAGTATGAAG	10260
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AACAGGAACA	CAAATTTCTC	AAAATTCCTG	CGATGTCCAA	TAAAGATTTT	CATAATTTCA	10440
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 AGGGTTAAGC GGACCAGGCA GGAGTAGCGG TTAAGTCAAGA GCAGGTCACA GGCTTGGGTT 10800  
 GTGAGGGTCA GGAGAGGCCA GGCCTCCTCG AGCAAGGTGG GGGTCCCAGG GTCAGGTCAG 10860  
 GTGCAGATCC TGTGGCAGCC ACGTCTTTCC ATGCTGGGCC TGCTGGGCCC CCCAGGCTTC 10920  
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 CAGGAGAGGA GGGCCTGGGG ACTGAGAGCA AGGGTCAGGG CCTCTCTTTG GGGAGGCCTC 11100  
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 GCATTTGCAG CTGTGCCATA TT 11722

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Gly Leu Gly Pro Val Phe Leu Leu Leu Ala Gly Ile Phe Pro Phe  
 1 5 10 15  
 Ala Pro Pro Gly Ala Ala Ala Glu Pro His Ser Leu Arg Tyr Asn Leu  
 20 25 30  
 Thr Val Leu Ser Trp Asp Gly Ser Val Gln Ser Gly Phe Leu Ala Glu  
 35 40 45



Val	His	Leu	Asp	Gly	Gln	Pro	Phe	Leu	Arg	Tyr	Asp	Arg	Gln	Lys	Cys	
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Arg	Ala	Lys	Pro	Gln	Gly	Gln	Trp	Ala	Glu	Asp	Val	Leu	Gly	Asn	Lys	
65					70					75					80	
Thr	Trp	Asp	Arg	Glu	Thr	Arg	Asp	Leu	Thr	Gly	Asn	Gly	Lys	Asp	Leu	
				85					90					95		
Arg	Met	Thr	Leu	Ala	His	Ile	Lys	Asp	Gln	Lys	Glu	Gly	Leu	His	Ser	
			100					105					110			
Leu	Gln	Glu	Ile	Arg	Val	Cys	Glu	Ile	His	Glu	Asp	Asn	Ser	Thr	Arg	
		115					120					125				
Ser	Ser	Gln	His	Phe	Tyr	Tyr	Asp	Gly	Glu	Leu	Phe	Leu	Ser	Gln	Asn	
	130					135					140					
Val	Glu	Thr	Glu	Glu	Trp	Thr	Val	Pro	Gln	Ser	Ser	Arg	Ala	Gln	Thr	
145					150					155					160	
Leu	Ala	Met	Asn	Val	Arg	Asn	Phe	Leu	Lys	Glu	Asp	Ala	Met	Lys	Thr	
			165						170					175		
Lys	Thr	His	Tyr	His	Ala	Met	His	Ala	Asp	Cys	Leu	Gln	Glu	Leu	Arg	
			180					185					190			
Arg	Tyr	Leu	Glu	Ser	Ser	Val	Val	Leu	Arg	Arg	Arg	Val	Pro	Pro	Met	
		195					200					205				
Val	Asn	Val	Thr	Arg	Ser	Glu	Ala	Ser	Glu	Gly	Asn	Ile	Thr	Val	Thr	
	210					215					220					
Cys	Arg	Ala	Ser	Ser	Phe	Tyr	Pro	Arg	Asn	Ile	Thr	Leu	Thr	Trp	Arg	
225					230					235					240	
Gln	Asp	Gly	Val	Ser	Leu	Ser	His	Asp	Thr	Gln	Gln	Trp	Gly	Asp	Val	
				245					250					255		
Leu	Pro	Asp	Gly	Asn	Gly	Thr	Tyr	Gln	Thr	Trp	Val	Ala	Thr	Arg	Ile	
			260					265					270			
Cys	Gln	Gly	Glu	Glu	Gln	Arg	Phe	Thr	Cys	Tyr	Met	Glu	His	Ser	Gly	
		275					280					285				
Asn	His	Ser	Thr	His	Pro	Val	Pro	Ser	Gly	Lys	Val	Leu	Val	Leu	Gln	
						295					300					
Ser	His	Trp	Gln	Thr	Phe	His	Val	Ser	Ala	Val	Ala	Ala	Ala	Ala	Ala	
305					310					315					320	
Ala	Ile	Phe	Val	Ile	Ile	Ile	Phe	Tyr	Val	Arg	Cys	Cys	Lys	Lys	Lys	
				325					330					335		
Thr	Ser	Ala	Ala	Glu	Gly	Pro	Glu	Leu	Val	Ser	Leu	Gln	Val	Leu	Asp	
			340					345					350			

Gln His Pro Val Gly Thr Ser Asp His Arg Asp Ala Thr Gln Leu Gly  
 355 360 365

Phe Gln Pro Leu Met Ser Ala Leu Gly Ser Thr Gly Ser Thr Glu Gly  
 370 375 380

Ala  
 385

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGCCATGGG GCTGGGCCGG GTCCTGCTGT TTCTGGCCGT CGCCTTCCCT TTTGCACCCC	60
CGGCAGCCGC CGCTGAGCCC CACAGTCTTC GTTACAACCT CATGGTGCTG TCCCAGGATG	120
AATCTGTGCA GTCAGGGTTT CTCGCTGAGG GACATCTGGA TGGTCAGCCC TTCCTGCGCT	180
ATGACAGGCA GAAACGCAGG GCAAAGCCCC AGGGACAGTG GGCAGAAGAT GTCCTGGGAG	240
CTAAGACCTG GGACACAGAG ACCGAGGACT TGACAGAGAA TGGGCAAGAC CTCAGGAGGA	300
CCCTGACTCA TATCAAGGAC CAGAAAGGAG GCTTGCATTC CCTCCAGGAG ATTAGGGTCT	360
GTGAGATCCA TGAAGACAGC AGCACCAGGG GCTCCCGGCA TTTCTACTAC GATGGGGAGC	420
TCTTCCTCTC CAAAACCTG GAGACTCAAG AATCGACAGT GCCCCAGTCC TCCAGAGCTC	480
AGACCTTGGC TATGAACGTC ACAAATTTCT GGAAGGAAGA TGCCATGAAG ACCAAGACAC	540
ACTATCGCGC TATGCAGGCA GACTGCCTGC AGAAACTACA GCGATATCTG AAATCCGGGG	600
TGGCCATCAG GAGAACAGTG CCCCCATGG TGAATGTCAC CTGCAGCGAG GTCTCAGAGG	660
GCAACATCAC CGTGACATGC AGGGCTTCCA GCTTCTATCC CCGGAATATC ACACTGACCT	720
GGCGTCAGGA TGGGGTATCT TTGAGCCACA ACACCCAGCA GTGGGGGGAT GTCCTGCCTG	780
ATGGGAATGG AACCTACCAG ACCTGGGTGG CCACCAGGAT TCGCCAAGGA GAGGAGCAGA	840
GGTTCACCTG CTACATGGAA CACAGCGGGA ATCACGGCAC TCACCCTGTG CCCTCTGGGA	900
AGGTGCTGGT GCTTCAGAGT CAACGGACAG ACTTTCCATA TGTTCCTGCT GCTATGCCAT	960
GTGTTGTTAT TATTATTATT CTCTGTGTCC CTGTGTGCAA GAAGAAAACA TCAGCGGCAG	1020
AGGGTCCAGA GCTTGTGAGC CTGCAGGTCC TGGATCAACA CCCAGTTGGG ACAGGAGACC	1080
ACAGGGATGC AGCACAGCTG GGATTTCAGC CTCTGATGTC AGCTACTGGG TCCACTGGTT	1140

CCACTGAGGG CGCCTAGACT CTACAGCCAG GCGGCCAGGA TTCAACTCCC TGCCTGGATC 1200  
 TCACCAGCAC TTTCCCTCTG TTTCCCTGACC TATGAAACAG AAAATAACAT CACTTATTTA 1260  
 TTGTTGTTGG ATGCTGCAAA GTGTTAGTAG GTATGAGGTG TTTGCTGCTC TGCCACGTAG 1320  
 AGAGCCAGCA AAGGGATCAT GACCAACTCA ACATTCCATT GGAGGCTATA TGATCAAACA 1380  
 GCAAATTGTT TATCATGAAT GCAGGATGTG GGCAAACTCA CGACTGCTCC TGCCAACAGA 1440  
 AGGTTTGCTG AGGGCATTCA CTCCATGGTG CTCATTGGAG TTATCTACTG GGTCACTAG 1500  
 AGCCTATTGT TTGAGGAATG CAGTCTTACA AGCCTACTCT GGACCCAGCA GCTGACTCCT 1560  
 TCTTCCACCC CTCTTCTG C TATCTCCTAT ACCAATAAAT ACGAAGGGCT GTGGAAGATC 1620  
 AGAGCCCTTG TTCACGAGAA GCAAGAAGCC CCCTGACCCC TTGTTCCAAA TATACTCTTT 1680  
 TGTCTTTCTC TTTATTCCCA CGTTCGCCCT TTGTTGAGTC CAATACAGGG TTGTGGGGCC 1740  
 CTTAACAGTG CCATATTAAT TGGTATCATT ATTTCTGTTG TTTTGTGTTT TGTTTTGTGTT 1800  
 TTGTTTGTG AGACAGAGTC TCACTCGTCA CCCAGGCTGC AGTTCACTGG TGTGATCTCA 1860  
 GCTCACTGCA ACCTCTGCCT CCCAGGTTCA AGCACTTCTC GTACCTCAGA CTCCCGATAG 1920  
 CTGGGATTAC AGACAGGCAC CACCACACCC AGCTAATTTT TGTATTTTTT GTAGAGACGG 1980  
 GGTTCGCCA AGTTGACCAG CCCAGTTTCA AACTCCTGAC CTCAGGTGAT CTGCCTGCCT 2040  
 TGGCATCCCA AAGTGCTGGG ATTACAAGAA TGAGCCACCG TGCCTGGCCT ATTTTATTAT 2100  
 ATTGTAATAT ATTTTATTAT ATTAGCCACC ATGCCTGTCC TATTTTCTTA TGTTTTAATA 2160  
 TATTTTAATA TATTACATGT GCAGTAATTA GATTATCATG GGTGAACTTT ATGAGTGAGT 2220  
 ATCTTGGTGA TGACTCCTCC TGACCAGCCC AGGACCAGCT TTCTTGTCAC CTTGAGGTCC 2280  
 CCTCGCCCCG TCACACCGTT ATCGATTACT CTGTGTCTAC TATTATGTGT GCATAATTTA 2340  
 TACCGTAAAT GTTTACTCTT TAAATAAAAA AAAAAAAAAA 2380

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Gly	Leu	Gly	Arg	Val	Leu	Leu	Phe	Leu	Ala	Val	Ala	Phe	Pro	Phe
1					5				10				15		
Ala	Pro	Pro	Ala	Ala	Ala	Ala	Glu	Pro	His	Ser	Leu	Arg	Tyr	Asn	Leu
			20				25						30		

Met Val Leu Ser Gln Asp Glu Ser Val Gln Ser Gly Phe Leu Ala Glu  
 35 40 45  
 Gly His Leu Asp Gly Gln Pro Phe Leu Arg Tyr Asp Arg Gln Lys Arg  
 50 55 60  
 Arg Ala Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Ala Lys  
 65 70 75 80  
 Thr Trp Asp Thr Glu Thr Glu Asp Leu Thr Glu Asn Gly Gln Asp Leu  
 85 90 95  
 Arg Arg Thr Leu Thr His Ile Lys Asp Gln Lys Gly Gly Leu His Ser  
 100 105 110  
 Leu Gln Glu Ile Arg Val Cys Glu Ile His Glu Asp Ser Ser Thr Arg  
 115 120 125  
 Gly Ser Arg His Phe Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn  
 130 135 140  
 Leu Glu Thr Gln Glu Ser Thr Val Pro Gln Ser Ser Arg Ala Gln Thr  
 145 150 155 160  
 Leu Ala Met Asn Val Thr Asn Phe Trp Lys Glu Asp Ala Met Lys Thr  
 165 170 175  
 Lys Thr His Tyr Arg Ala Met Gln Ala Asp Cys Leu Gln Lys Leu Gln  
 180 185 190  
 Arg Tyr Leu Lys Ser Gly Val Ala Ile Arg Arg Thr Val Pro Pro Met  
 195 200 205  
 Val Asn Val Thr Cys Ser Glu Val Ser Glu Gly Asn Ile Thr Val Thr  
 210 215 220  
 Cys Arg Ala Ser Ser Phe Tyr Pro Arg Asn Ile Thr Leu Thr Trp Arg  
 225 230 235 240  
 Gln Asp Gly Val Ser Leu Ser His Asn Thr Gln Gln Trp Gly Asp Val  
 245 250 255  
 Leu Pro Asp Gly Asn Gly Thr Tyr Gln Thr Trp Val Ala Thr Arg Ile  
 260 265 270  
 Arg Gln Gly Glu Glu Gln Arg Phe Thr Cys Tyr Met Glu His Ser Gly  
 275 280 285  
 Asn His Gly Thr His Pro Val Pro Ser Gly Lys Val Leu Val Leu Gln  
 290 295 300  
 Ser Gln Arg Thr Asp Phe Pro Tyr Val Ser Ala Ala Met Pro Cys Phe  
 305 310 315 320  
 Val Ile Ile Ile Ile Leu Cys Val Pro Cys Cys Lys Lys Lys Thr Ser  
 325 330 335

Ala Ala Glu Gly Pro Glu Leu Val Ser Leu Gln Val Leu Asp Gln His  
 340 345 350

Pro Val Gly Thr Gly Asp His Arg Asp Ala Ala Gln Leu Gly Phe Gln  
 355 360 365

Pro Leu Met Ser Ala Thr Gly Ser Thr Gly Ser Thr Glu Gly Ala  
 370 375 380

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACTGGGGAAC AAGGTTTATA TGAGA

25

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TGTCACCCGT CTTCTACAGG ACCC

24

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGGGCCATGG GGCTGGG

17

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ATCTGAGATG TCGGTCC

17

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGTTCTTGTC CCTTTGCCCCG TGTGC

25

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AACCCTTCCC TTACCCCGT CGTAG

25

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TATGTAAAC GACGGCCAGT TTCACCTGTG ATTTCCTCTT CCCCA

45

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGTCTTTTCA ATCCCCGTCT CTCGTCCAGT ATCGACAAAG GACAT

45

(2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TATGTAAAC GACGGCCAGT TTCGGAATG GAGAAGTCAC

40

## (2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CGAGAGGAGA GGGAGGTAA CCAGTATCGA CAAAGGACAT

40

## (2) INFORMATION FOR SEQ ID NO: 15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TATGTAAAC GACGGCCAGT GTTCCTCTCC CTCCTTAGA

40

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AAAAAGTCCC TTTCACGACC ACCAGTATCG ACAAAGGACA T

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